



PCT10

## RAW SEQUENCE LISTING

DATE: 04/01/2005

PATENT APPLICATION: US/10/528,611

TIME: 15:52:37

Input Set : N:\AMC\528611.txt

Output Set: N:\CRF4\04012005\J528611.raw

3 <110> APPLICANT: E. I. du Pont de Nemours and Company  
 5 <120> TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
 7 <130> FILE REFERENCE: BB1533 PCT  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/528,611  
 C--> 9 <141> CURRENT FILING DATE: 2005-03-21  
 9 <150> PRIOR APPLICATION NUMBER: 60/412,795  
 10 <151> PRIOR FILING DATE: 2002-09-23  
 12 <150> PRIOR APPLICATION NUMBER: 60/427,324  
 13 <151> PRIOR FILING DATE: 2002-11-18  
 15 <160> NUMBER OF SEQ ID NOS: 149  
 17 <170> SOFTWARE: PatentIn version 3.1  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 15679  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Heliothis virescens  
 24 <220> FEATURE:  
 25 <221> NAME/KEY: CDS  
 26 <222> LOCATION: (251)..(15676)  
 27 <223> OTHER INFORMATION:  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: misc\_feature  
 31 <222> LOCATION: (5515)  
 32 <223> OTHER INFORMATION: n = c or g  
 W--> 34 <220>  
 35 <221> NAME/KEY: misc\_feature  
 36 <222> LOCATION: (13000)  
 37 <223> OTHER INFORMATION: n = a or t  
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 41 ttatgggacg tgtgattatt ccgaatttag aatcattagt gttgtgaacg gttaaaaatg 120  
 42 tgттаacagt gcgtgcagcg ttgattccag aaaaaacgga tttatttgtg cgttttgacg 180  
 43 catgtgtgat gcatttcgag tgttatggca acgttgcagt aaggcactga cagtctactg 240  
 44 agaatccaag atg gcg gaa gca gag ggg gga gca agc gag caa gat gat 289  
 45 Met Ala Glu Ala Glu Gly Gly Ala Ser Glu Gln Asp Asp  
 46 1 5 10  
 47 gtt tca atc ttg cgt acg gaa gac atg gtg tgc atg tcg tgc aca gcg 337  
 48 Val Ser Ile Leu Arg Thr Glu Asp Met Val Cys Met Ser Cys Thr Ala  
 49 15 20 25  
 50 aca gga gag agg gtg tgc ctg gct gcc gaa ggt ctc ggc aac cgg cac 385  
 51 Thr Gly Glu Arg Val Cys Leu Ala Ala Glu Gly Leu Gly Asn Arg His  
 52 30 35 40 45  
 53 tgc ttc ctg gag aat att gcc gac aag aac ata ccg cct gat ctg tcg 433  
 54 Cys Phe Leu Glu Asn Ile Ala Asp Lys Asn Ile Pro Pro Asp Leu Ser

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55	50	55	60	
56	cag tgt gtg ttt gtc atc gaa cag gcg ctt tca gta aga gct tta cag	481		
59	Gln Cys Val Phe Val Ile Glu Gln Ala Leu Ser Val Arg Ala Leu Gln			
60	65 70 75			
61	gag ttg gta aca gct gcg gga tct gaa act ggg aaa gaa aac tta ggt	529		
62	Glu Leu Val Thr Ala Ala Gly Ser Glu Thr Gly Lys Glu Asn Leu Gly			
63	80 85 90			
64	aaa ggt acc ggt tct ggt tat cgt acg cta cta tac ggc aat gct att	577		
65	Lys Gly Thr Gly Ser Gly Tyr Arg Thr Leu Leu Tyr Gly Asn Ala Ile			
66	95 100 105			
67	ctt ttg cga cat ctt aac agt gat atg tac ctg gcc tgc ctg tca aca	625		
68	Leu Leu Arg His Leu Asn Ser Asp Met Tyr Leu Ala Cys Leu Ser Thr			
69	110 115 120 125			
70	tca tca tcc cag gat aag ctg gcc ttt gac gtg ggt ctg caa cag cac	673		
71	Ser Ser Ser Gln Asp Lys Leu Ala Phe Asp Val Gly Leu Gln Gln His			
72	130 135 140			
73	tcc caa ggt gaa gcc tgc tgg tgg acc ctg cat cct gcc agc aaa cag	721		
74	Ser Gln Gly Glu Ala Cys Trp Trp Thr Leu His Pro Ala Ser Lys Gln			
75	145 150 155			
76	aga tcc gag ggc gag aag gtg cga gtc gga gat gac ttg att cta gtc	769		
77	Arg Ser Glu Gly Glu Lys Val Arg Val Gly Asp Asp Leu Ile Leu Val			
78	160 165 170			
79	tcc gtg gcc att gag aga tac ttg cac aca acg aaa gag aac gaa gta	817		
80	Ser Val Ala Ile Glu Arg Tyr Leu His Thr Thr Lys Glu Asn Glu Val			
81	175 180 185			
82	tcg ata gtg aac gcg tcg ttc cac gtg acg cac tgg tcg gta cag ccc	865		
83	Ser Ile Val Asn Ala Ser Phe His Val Thr His Trp Ser Val Gln Pro			
84	190 195 200 205			
85	tat ggt act ggt ata tcg agg atg aag tat gtg ggc tat gtg ttc gga	913		
86	Tyr Gly Thr Gly Ile Ser Arg Met Lys Tyr Val Gly Tyr Val Phe Gly			
87	210 215 220			
88	ggt gat gtg ctc agg ttc ttc cat gga ggt gac gag tgt ctc act ata	961		
89	Gly Asp Val Leu Arg Phe Phe His Gly Gly Asp Glu Cys Leu Thr Ile			
90	225 230 235			
91	cct agc act tgg aca aag gat ggg ggg caa aat atc gta gtc tac aaa	1009		
92	Pro Ser Thr Trp Thr Lys Asp Gly Gly Gln Asn Ile Val Val Tyr Lys			
93	240 245 250			
94	gga ggt tca gtg atg tct caa gcc cgt tct cta tgg cgc ctg gag ctg	1057		
95	Gly Gly Ser Val Met Ser Gln Ala Arg Ser Leu Trp Arg Leu Glu Leu			
96	255 260 265			
97	gct aga acc aag tgg gcc gga ggt ttc att aac tgg tac cat cct atg	1105		
98	Ala Arg Thr Lys Trp Ala Gly Gly Phe Ile Asn Trp Tyr His Pro Met			
99	270 275 280 285			
100	agg att cgg cac atc act act gga aga tat ctt gga gtt aac gac cag	1153		
101	Arg Ile Arg His Ile Thr Thr Gly Arg Tyr Leu Gly Val Asn Asp Gln			
102	290 295 300			
103	aat gag ctg tat tta gtt agc aga gag gaa ccc aca aca gct tcc tgt	1201		
104	Asn Glu Leu Tyr Leu Val Ser Arg Glu Glu Pro Thr Thr Ala Ser Cys			
105	305 310 315			

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106	gcc	ttc	tgc	ctg	cgc	cag	gag	aag	gat	gat	cag	aag	caa	gtg	tta	gaa	1249
107	Ala	Phe	Cys	Leu	Arg	Gln	Glu	Lys	Asp	Asp	Gln	Lys	Gln	Val	Leu	Glu	
108			320					325					330				
109	gac	aag	gac	ttg	gag	gtc	ata	ggc	gcg	ccc	atc	atc	aag	tac	ggt	gac	1297
110	Asp	Lys	Asp	Leu	Glu	Val	Ile	Gly	Ala	Pro	Ile	Ile	Lys	Tyr	Gly	Asp	
111		335					340					345					
112	tcc	acc	gtc	att	gtg	cag	cat	tcg	gag	act	ggc	ttg	tgg	ctg	tct	tat	1345
113	Ser	Thr	Val	Ile	Val	Gln	His	Ser	Glu	Thr	Gly	Leu	Trp	Leu	Ser	Tyr	
114	350					355					360					365	
115	aag	tct	tac	gaa	acg	aag	aag	aaa	ggc	gtg	ggt	aaa	gta	gaa	gag	aag	1393
116	Lys	Ser	Tyr	Glu	Thr	Lys	Lys	Lys	Gly	Val	Gly	Lys	Val	Glu	Glu	Lys	
117					370						375					380	
118	caa	gcg	att	ctc	cac	gag	gaa	ggc	aag	atg	gac	gat	ggc	ctc	gac	ctc	1441
119	Gln	Ala	Ile	Leu	His	Glu	Glu	Gly	Lys	Met	Asp	Asp	Gly	Leu	Asp	Leu	
120					385				390							395	
121	tcc	agg	tca	cag	gag	gaa	gaa	tct	atg	act	gct	cga	gtt	atc	agg	aag	1489
122	Ser	Arg	Ser	Gln	Glu	Glu	Glu	Ser	Met	Thr	Ala	Arg	Val	Ile	Arg	Lys	
123			400					405					410				
124	tgt	tct	tcg	ctg	ttc	act	aag	ttt	atc	aat	ggc	ctg	gaa	act	ctt	caa	1537
125	Cys	Ser	Ser	Leu	Phe	Thr	Lys	Phe	Ile	Asn	Gly	Leu	Glu	Thr	Leu	Gln	
126			415					420					425				
127	gag	aac	cgt	cgt	cac	tcg	atg	ttc	ttc	gcg	tca	gtg	aac	ctg	ggc	gag	1585
128	Glu	Asn	Arg	Arg	His	Ser	Met	Phe	Phe	Ala	Ser	Val	Asn	Leu	Gly	Glu	
129	430					435					440					445	
130	atg	gtg	atg	tgt	ctt	gaa	gat	ctc	acc	aac	tac	ttc	gca	cag	ccc	gat	1633
131	Met	Val	Met	Cys	Leu	Glu	Asp	Leu	Thr	Asn	Tyr	Phe	Ala	Gln	Pro	Asp	
132					450						455					460	
133	gag	gat	atg	gaa	cac	gaa	gaa	aag	caa	aac	aaa	ttc	cgc	gcc	ctc	cgc	1681
134	Glu	Asp	Met	Glu	His	Glu	Glu	Lys	Gln	Asn	Lys	Phe	Arg	Ala	Leu	Arg	
135					465				470							475	
136	aac	cgt	cag	gac	ctg	ttc	caa	gag	gaa	ggc	ata	ctg	aac	ctg	atc	ctc	1729
137	Asn	Arg	Gln	Asp	Leu	Phe	Gln	Glu	Gly	Ile	Leu	Asn	Leu	Ile	Leu		
138			480					485					490				
139	gaa	gct	ata	gac	aag	atc	aac	gtc	gtc	acg	tcc	cag	ggg	ttc	ctg	gct	1777
140	Glu	Ala	Ile	Asp	Lys	Ile	Asn	Val	Val	Thr	Ser	Gln	Gly	Phe	Leu	Ala	
141			495				500						505				
142	gga	ttc	ctg	gcg	gga	gac	gaa	tct	gga	cag	agc	tgg	gaa	atg	ata	tct	1825
143	Gly	Phe	Leu	Ala	Gly	Asp	Glu	Ser	Gly	Gln	Ser	Trp	Glu	Met	Ile	Ser	
144	510					515					520					525	
145	gga	tat	ttg	tat	cag	ttg	ctg	gcg	gca	ata	ata	aaa	ggc	aac	cac	acg	1873
146	Gly	Tyr	Leu	Tyr	Gln	Leu	Leu	Ala	Ala	Ile	Ile	Lys	Gly	Asn	His	Thr	
147					530						535					540	
148	aac	tgc	gcg	cag	ttc	gcg	aac	tcg	aac	cgg	ttc	aac	tgg	ctg	ttc	tcg	1921
149	Asn	Cys	Ala	Gln	Phe	Ala	Asn	Ser	Asn	Arg	Phe	Asn	Trp	Leu	Phe	Ser	
150					545					550						555	
151	cgc	ctc	ggc	tcg	cag	gcc	tcg	ggc	gag	ggc	acc	ggc	atg	ctc	gac	gtg	1969
152	Arg	Leu	Gly	Ser	Gln	Ala	Ser	Gly	Glu	Gly	Thr	Gly	Met	Leu	Asp	Val	
153			560					565					570				
154	ctg	cac	tgc	atc	ctc	atc	gac	tcg	cct	gaa	gcg	ctc	aac	atg	atg	agg	2017

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155	Leu	His	Cys	Ile	Leu	Ile	Asp	Ser	Pro	Glu	Ala	Leu	Asn	Met	Met	Arg	
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157	gac	gaa	cac	ata	aaa	gtg	ata	atc	tct	cta	tta	gaa	aag	cac	gga	cgc	2065
158	Asp	Glu	His	Ile	Lys	Val	Ile	Ile	Ser	Leu	Leu	Glu	Lys	His	Gly	Arg	
159	590					595					600					605	
160	gac	cct	aaa	gta	cta	gat	gtg	cta	tgt	tca	ctc	tgc	gtc	ggc	aac	ggc	2113
161	Asp	Pro	Lys	Val	Leu	Asp	Val	Leu	Cys	Ser	Leu	Cys	Val	Gly	Asn	Gly	
162					610					615					620		
163	gtc	gcg	gtg	cgc	tcg	tca	cag	aac	aac	atc	tgc	gac	tat	ttg	ctg	ccc	2161
164	Val	Ala	Val	Arg	Ser	Ser	Gln	Asn	Asn	Ile	Cys	Asp	Tyr	Leu	Leu	Pro	
165				625					630					635			
166	ggc	aag	aac	ctg	ttg	ctg	caa	act	gcg	ctt	gta	gat	cac	gta	tct	agt	2209
167	Gly	Lys	Asn	Leu	Leu	Leu	Gln	Thr	Ala	Leu	Val	Asp	His	Val	Ser	Ser	
168			640					645					650				
169	gtc	cgt	ccg	aac	atc	ttc	gtg	ggc	cga	gta	gaa	ggg	tcg	gca	gtg	tac	2257
170	Val	Arg	Pro	Asn	Ile	Phe	Val	Gly	Arg	Val	Glu	Gly	Ser	Ala	Val	Tyr	
171		655					660					665					
172	cgc	aaa	tgg	tac	ttc	gag	gtg	act	atg	gac	cac	ata	gag	aag	acc	aca	2305
173	Arg	Lys	Trp	Tyr	Phe	Glu	Val	Thr	Met	Asp	His	Ile	Glu	Lys	Thr	Thr	
174	670				675					680						685	
175	cat	atg	atg	cca	cat	cta	cgc	ata	gga	tgg	gct	aac	act	act	ggc	tat	2353
176	His	Met	Met	Pro	His	Leu	Arg	Ile	Gly	Trp	Ala	Asn	Thr	Thr	Gly	Tyr	
177				690						695					700		
178	gtc	cca	tac	ccg	ggc	ggc	ggc	gag	aag	tgg	gga	ggc	aac	ggc	gtg	gga	2401
179	Val	Pro	Tyr	Pro	Gly	Gly	Gly	Glu	Lys	Trp	Gly	Gly	Asn	Gly	Val	Gly	
180				705						710				715			
181	gac	gac	ctg	tac	tcg	tac	ggg	ttt	gat	ggc	gcc	tac	ctc	tgg	tcc	ggc	2449
182	Asp	Asp	Leu	Tyr	Ser	Tyr	Gly	Phe	Asp	Gly	Ala	Tyr	Leu	Trp	Ser	Gly	
183			720				725					730					
184	ggg	agg	aag	acc	ccg	gtc	aat	agg	act	cat	gct	gaa	gag	cct	tat	att	2497
185	Gly	Arg	Lys	Thr	Pro	Val	Asn	Arg	Thr	His	Ala	Glu	Glu	Pro	Tyr	Ile	
186		735					740					745					
187	agg	aaa	ggc	gac	gtg	ata	ggc	tgt	gca	ttg	gac	ctg	acg	gta	ccc	atc	2545
188	Arg	Lys	Gly	Asp	Val	Ile	Gly	Cys	Ala	Leu	Asp	Leu	Thr	Val	Pro	Ile	
189	750				755					760						765	
190	atc	aac	ttc	atg	ttc	aac	gga	gtg	cgg	gtg	acg	gga	tcc	ttc	acc	aac	2593
191	Ile	Asn	Phe	Met	Phe	Asn	Gly	Val	Arg	Val	Thr	Gly	Ser	Phe	Thr	Asn	
192				770						775					780		
193	ttc	aat	ctg	gaa	ggc	atg	ttc	ttc	ccg	gtc	atc	agc	tgc	tct	agt	aag	2641
194	Phe	Asn	Leu	Glu	Gly	Met	Phe	Phe	Pro	Val	Ile	Ser	Cys	Ser	Ser	Lys	
195			785						790					795			
196	ctg	agt	tgt	cgg	ttc	ctg	ctg	ggc	gga	gaa	cac	ggc	aga	ctc	cgg	tac	2689
197	Leu	Ser	Cys	Arg	Phe	Leu	Leu	Gly	Gly	Glu	His	Gly	Arg	Leu	Arg	Tyr	
198		800						805					810				
199	gcg	gct	cca	gaa	ggc	tac	tcc	ccg	ctg	gtg	gag	tct	ctc	ctg	ccg	cag	2737
200	Ala	Ala	Pro	Glu	Gly	Tyr	Ser	Pro	Leu	Val	Glu	Ser	Leu	Leu	Pro	Gln	
201		815					820					825					
202	cag	atc	ctc	agc	ctg	gag	ccg	tgc	ttc	tac	ttc	ggc	aac	ctg	tcc	aag	2785
203	Gln	Ile	Leu	Ser	Leu	Glu	Pro	Cys	Phe	Tyr	Phe	Gly	Asn	Leu	Ser	Lys	

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204	830		835		840		845	
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206	Arg Ala Leu Ala Gly Pro Pro Leu Val Gln Asp Asp Thr Ala Phe Val							
207		850		855		860		
208	cct acg cct gtt gat act tta cag att act ctg cct aca tat gtg gaa							2881
209	Pro Thr Pro Val Asp Thr Leu Gln Ile Thr Leu Pro Thr Tyr Val Glu							
210		865		870		875		
211	caa atc aga gac aag cta gct gaa aat att cac gaa atg tgg gct atg							2929
212	Gln Ile Arg Asp Lys Leu Ala Glu Asn Ile His Glu Met Trp Ala Met							
213		880		885		890		
214	aat aag atc gaa gca ggc tgg atg tac ggc gac cag aga gaa gac ttg							2977
215	Asn Lys Ile Glu Ala Gly Trp Met Tyr Gly Asp Gln Arg Glu Asp Leu							
216		895		900		905		
217	cac aag atc cac ccc tgc ctc gtg ccc ttc gag cga ctc ccg ccc gct							3025
218	His Lys Ile His Pro Cys Leu Val Pro Phe Glu Arg Leu Pro Pro Ala							
219	910		915		920		925	
220	gag aaa cga tac gat ata caa ctt gct gtg cag aca ctc aag act atc							3073
221	Glu Lys Arg Tyr Asp Ile Gln Leu Ala Val Gln Thr Leu Lys Thr Ile							
222		930		935		940		
223	ctg gct ctg ggc tac tac atc agc tta gat aag cct cca gca cgc atc							3121
224	Leu Ala Leu Gly Tyr Tyr Ile Ser Leu Asp Lys Pro Pro Ala Arg Ile							
225		945		950		955		
226	cgc aac gtt cgt ctg ccc aat gaa cct ttc atg cag tcc aac ggc tac							3169
227	Arg Asn Val Arg Leu Pro Asn Glu Pro Phe Met Gln Ser Asn Gly Tyr							
228		960		965		970		
229	aag cca gca cca ctc gac ctg agt gct gtc acc ctg aca ccc aag atg							3217
230	Lys Pro Ala Pro Leu Asp Leu Ser Ala Val Thr Leu Thr Pro Lys Met							
231		975		980		985		
232	gat gag cta gta ggc cag ctg gct gag aac acc cac aac ctt tgg gcc							3265
233	Asp Glu Leu Val Gly Gln Leu Ala Glu Asn Thr His Asn Leu Trp Ala							
234	990		995		1000		1005	
235	agg gag agg ata cag cag gga tgg act tac gga ctt aat gag gac							3310
236	Arg Glu Arg Ile Gln Gln Gly Trp Thr Tyr Gly Leu Asn Glu Asp							
237		1010		1015		1020		
238	tcg gac atg cat cga tcc ccg cac ctg gtg cca tac ccg aag gtt							3355
239	Ser Asp Met His Arg Ser Pro His Leu Val Pro Tyr Pro Lys Val							
240		1025		1030		1035		
241	gac gat gcc atc aag aag gcc aac agg gac aca gcc tcg gag act							3400
242	Asp Asp Ala Ile Lys Lys Ala Asn Arg Asp Thr Ala Ser Glu Thr							
243		1040		1045		1050		
244	gtg agg acc ctg ctg gtc tac ggg tat atg ctg gac ccg cct act							3445
245	Val Arg Thr Leu Leu Val Tyr Gly Tyr Met Leu Asp Pro Pro Thr							
246		1055		1060		1065		
247	ggg gag cag cat gaa gca ctc ttg ttg gaa gcg tca aaa cag aag							3490
248	Gly Glu Gln His Glu Ala Leu Leu Leu Glu Ala Ser Lys Gln Lys							
249		1070		1075		1080		
250	caa gcc gac ttc aga aca tac cgc gct gag aag aac tat gcc gtc							3535
251	Gln Ala Asp Phe Arg Thr Tyr Arg Ala Glu Lys Asn Tyr Ala Val							
252		1085		1090		1095		

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 5515,13000  
Seq#:1; Xaa Pos. 1755,4250  
Seq#:2; Xaa Pos. 1755,4250  
Seq#:3; N Pos. 36,37,5807  
Seq#:7; N Pos. 1264  
Seq#:7; Xaa Pos. 416  
Seq#:8; Xaa Pos. 416  
Seq#:9; N Pos. 15890  
Seq#:11; N Pos. 6,9,10,12,15  
Seq#:12; N Pos. 9,12,13,15,18  
Seq#:13; N Pos. 9,12,15,18  
Seq#:14; N Pos. 6,9,12,18,21  
Seq#:15; N Pos. 6,9,12,15,18  
Seq#:16; N Pos. 9,12,15,16,17,18  
Seq#:17; N Pos. 9,12,15,18  
Seq#:18; N Pos. 6,9,12  
Seq#:19; N Pos. 9,12,15,18  
Seq#:20; N Pos. 5,9,12,15,18  
Seq#:21; N Pos. 11,12,15,18  
Seq#:22; N Pos. 9,12,15,18,21  
Seq#:27; N Pos. 9,12,15,18  
Seq#:28; N Pos. 9,12,15,18  
Seq#:29; N Pos. 3,6,9,12,15,18  
Seq#:30; N Pos. 3,6,9,12,18  
Seq#:63; Xaa Pos. 16,22,31,37  
Seq#:64; Xaa Pos. 14,23  
Seq#:66; Xaa Pos. 16,23  
Seq#:67; Xaa Pos. 8,11  
Seq#:68; Xaa Pos. 20  
Seq#:69; Xaa Pos. 9  
Seq#:70; Xaa Pos. 10,11,26  
Seq#:72; Xaa Pos. 9,21  
Seq#:73; Xaa Pos. 10  
Seq#:74; Xaa Pos. 12  
Seq#:75; Xaa Pos. 7  
Seq#:76; Xaa Pos. 8  
Seq#:77; Xaa Pos. 9,13  
Seq#:78; Xaa Pos. 6  
Seq#:79; Xaa Pos. 4  
Seq#:80; Xaa Pos. 10  
Seq#:81; Xaa Pos. 10  
Seq#:82; Xaa Pos. 9  
Seq#:83; Xaa Pos. 11,17  
Seq#:84; Xaa Pos. 7,19,23,32

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Seq#:85; Xaa Pos. 8,24,26

Seq#:86; Xaa Pos. 37

Seq#:87; Xaa Pos. 21,46

Seq#:88; Xaa Pos. 13

Seq#:90; Xaa Pos. 12

Seq#:91; Xaa Pos. 11,15

Seq#:93; Xaa Pos. 12

## VERIFICATION SUMMARY

DATE: 04/01/2005

PATENT APPLICATION: US/10/528,611

TIME: 15:52:38

Input Set : N:\AMC\528611.txt

Output Set: N:\CRF4\04012005\J528611.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:34 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:27  
L:382 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:5470  
M:341 Repeated in SeqNo=1  
L:1304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:1743  
M:341 Repeated in SeqNo=2  
L:1777 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0  
M:341 Repeated in SeqNo=3  
L:3070 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:3068  
L:4779 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:4777  
L:4858 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:1252  
M:341 Repeated in SeqNo=7  
L:5884 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:400  
L:6839 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:6837  
L:8195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:15837  
L:9262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0  
L:9304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0  
L:9338 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0  
L:9379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0  
L:9420 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0  
L:9467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0  
L:9502 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0  
L:9531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0  
L:9566 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0  
L:9607 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0  
L:9642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0  
L:9684 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0  
L:9767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0  
L:9803 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0  
L:9851 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0  
L:9893 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0  
L:17247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63 after pos.:0  
M:341 Repeated in SeqNo=63  
L:17276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64 after pos.:0  
M:341 Repeated in SeqNo=64  
L:17291 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:65,Line#:17289  
L:17318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66 after pos.:0  
M:341 Repeated in SeqNo=66  
L:17341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67 after pos.:0  
L:17362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68 after pos.:16  
L:17378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69 after pos.:0  
L:17406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70 after pos.:0  
M:341 Repeated in SeqNo=70  
L:17424 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:71,Line#:17422  
L:17448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72 after pos.:0  
M:341 Repeated in SeqNo=72  
L:17475 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73 after pos.:0



## VERIFICATION SUMMARY

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L:17493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74 after pos.:0  
L:17511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75 after pos.:0  
L:17527 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:0  
L:17550 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77 after pos.:0  
L:17568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78 after pos.:0  
L:17583 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79 after pos.:0  
L:17598 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80 after pos.:0  
L:17617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81 after pos.:0  
L:17635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82 after pos.:0  
L:17659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:0  
L:17812 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:89,Line#:17810  
L:17873 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:92,Line#:17871  
L:17922 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:95,Line#:17920  
L:17935 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:96,Line#:17933  
L:18025 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:101,Line#:18023  
L:18074 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:104,Line#:18072  
L:18090 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:105,Line#:18088  
L:18221 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:110,Line#:18219  
L:18276 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:113,Line#:18274  
L:18292 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:114,Line#:18290  
L:18389 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:118,Line#:18387  
L:18405 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:119,Line#:18403  
L:25588 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:127,Line#:25583  
L:27979 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:129,Line#:27974  
L:30526 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:143,Line#:30521  
L:32924 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:145,Line#:32919